

Amendments to the Claims:

In the claims:

Claims 1-59. (canceled)

60. (currently amended) A computer system comprising:

- (a) a database comprising quantitative gene expression information from a liver cell or tissue sample exposed to at least one hepatotoxin and quantitative gene expression information from a liver cell or tissue sample exposed to the hepatotoxin excipient; ~~and~~
- (b) software that allows a user to compare quantitative gene expression information obtained from a liver cell or tissue sample exposed to a test agent to the quantitative gene expression information in the database to predict whether the test agent is a hepatotoxin; ~~and~~
- (c) a user interface to display or provide the results of said comparison.

61. (previously presented) A computer system of claim 60, wherein the database further comprises sequence information for at least one gene.

62. (previously presented) A computer system of claim 60, wherein the database further comprises information identifying the expression level of at least one gene in the tissue or cell sample before exposure to a toxin.

63. (previously presented) A computer system of claim 60, wherein the database further comprises information identifying the expression level of at least one gene in a tissue or cell sample exposed to at least a second toxin.

64. (previously presented) A computer system of claim 60, wherein the database further comprises records including descriptive information from an external database, which information correlates at least one gene to records in the external database.

65. (previously presented) A computer system of claim 64, wherein the external database is GenBank[®].

66. (previously presented) A computer system of claim 60, wherein the information comprises at least one mean expression value from a gene in a toxin exposed cell or tissue sample group.

67. (previously presented) A computer system of claim 66, wherein the information further comprises a mean expression value from a gene in a control cell or tissue sample group.

68. (previously presented) A computer system of claim 67, wherein the information further comprises a discriminant score for at least one gene.

69. (previously presented) A computer system of claim 60, wherein the information comprises a toxicity model and wherein each gene in the model predicts whether a cell or tissue sample has been exposed to a toxin.

70. (currently amended) A computer system of claim 69, wherein the model is selected from the group consisting of a general hepatotoxicity model, an individual hepatotoxin model and a liver pathology model.

71. (previously presented) A computer system of claim 67, wherein the control group was exposed to a delivery vehicle, a low dose of the toxin or an unrelated toxin.

72. (currently amended) A computer system of claim 60, wherein the individual toxin model is selected from the group consisting of acyclovir, amitryptiline, alpha-naphthylisothiocyanate (ANIT), acetaminophen, AY-25329, bicalutamide, carbon tetrachloride, clofibrate, cyproterone acetate (CPA), diclofenac, diflunisal, dioxin, 17 α -ethinylestradiol, hydrazine, indomethacin, lipopolysaccharide, phenobarbital, tacrine, valproate, WY-14643 and zileuton models.

73. (previously presented) A computer system of claim 60, wherein the genes are rat genes.

74. (previously presented) A computer system of claim 73, wherein the database comprises the information of any one of Tables 3A-3DD.

75–87. (canceled)

88. (currently amended). A method of using a computer system of claim 60 to predict a toxic response in a liver cell or tissue sample exposed to a test agent, comprising,

(a) comparing a gene expression profile from the liver cell or tissue sample exposed to the test agent to information in the database; and

(b) displaying information indicating at least one gene whose expression levels are up- or down-regulated upon exposure to the test agent, thereby predicting a toxic response in the liver cell or tissue sample.

89. (previously presented) A method of claim 88, wherein expression levels of at least two genes in the gene expression profile are compared to information in the database.

90. (previously presented) A method of claim 88, wherein expression levels of at least five genes in the gene expression profile are compared to information in the database.

91. (previously presented) A method of claim 88, wherein expression levels of at least ten genes in the gene expression profile are compared to information in the database.

92. (previously presented) A method of claim 88, wherein expression levels of all the genes in the gene expression profile are compared to information in the database.

93. (canceled)

94. (previously presented) A computer system of claim 60, wherein the database is stored on at least one computer-readable medium.

95. (previously presented) A computer system of claim 60, wherein the database comprises quantitative gene expression information for at least 10 genes of tables 3A-DD.

96. (previously presented) A computer system of claim 60, wherein the database comprises quantitative gene expression information for at least 50 genes of tables 3A-DD.

97. (previously presented) A computer system of claim 60, wherein the database comprises quantitative gene expression information for at least 100 genes of tables 3A-DD.

98. (currently amended) A computer readable medium comprising:

(a) a database comprising quantitative gene expression information from a liver cell or tissue sample exposed to at least one hepatotoxin and quantitative gene expression information from a liver cell or tissue sample exposed to the hepatotoxin excipient; and

(b) software that allows a user to compare quantitative gene expression information obtained from a liver cell or tissue sample exposed to a test agent to the quantitative gene expression information in the database to predict whether the test agent is a toxin; ~~and~~
operably linked to a user interface to display or provide the results of said comparison.

99. (previously presented) A computer readable medium of claim 98, wherein the database further comprises sequence information for the at least one gene.

100. (previously presented) A computer readable medium of claim 98, wherein the database further comprises information identifying the expression level for at least one gene in the tissue or cell sample before exposure to a toxin.

101. (previously presented) A computer readable medium of claim 98, wherein the database further comprises information identifying the expression level of at least one gene in a tissue or cell sample exposed to at least a second toxin.

102. (previously presented) A computer readable medium of claim 98, wherein the database further comprises at least one mean expression value for a gene in a toxin-exposed cell or tissue sample group.

103. (previously presented) A computer readable medium of claim 98, wherein the database further comprises at least one mean expression value for a gene in a control cell or tissue sample group.

104. (previously presented) A computer readable medium of claim 98, wherein the database further comprises at least one discriminant score for a gene in a toxin -exposed cell or tissue sample group.

105. (previously presented) A computer readable medium of claim 98, wherein the database further comprises a toxicity model and wherein each gene in the model predicts whether a cell or tissue sample has been exposed to a toxin.

106. (currently amended) A computer readable medium of claim 98, wherein the model is selected from the group consisting of a general hepatotoxicity model, an individual hepatotoxin model and a liver pathology model.

107. (previously presented) A computer readable medium of claim 103, wherein the control group was exposed to a delivery vehicle, a low dose of the toxin or an unrelated toxin.

108. (currently amended) A computer readable medium of claim 106, wherein the individual hepatotoxin ~~model~~ is selected from the group consisting of acyclovir, amitryptiline, alpha-naphthylisothiocyante (ANIT), acetaminophen, AY-25329, bicalutamide, carbon tetrachloride, clofibrate, cyproterone acetate (CPA), diclofenac, diflunisal, dioxin, 17 α -ethinylestradiol, hydrazine, indomethacin, lipopolysaccharide, phenobarbital, tacrine, valproate, WY-14643 and zileuton.

109. (previously presented) A computer readable medium of claim 98, wherein the genes are rat genes.

110. (previously presented) A computer readable medium of claim 98, wherein the database comprises the information of any one of Tables 3A-3DD.